Sequence Listing

<110> Adams, Sean
Pan, James
Zhong, Alan

<120> UCP4

<130> P1626R1

<140> US 09/397,342
<141> 1999-09-15

<150> US 60/101,279
<151> 1998-09-22

<150> US 60/114,223
<151> 1998-12-30

<150> US 60/129,674
<151> 1999-04-16

<160> 18

<210> 1
<211> 323
<212> PRT
<213> Homo sapiens

<400> 1

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 Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
   1               5                  10                  15

 Arg Trp Pro Arg Ala Ser Lys Phe Leu Leu Ser Gly Cys Ala Ala
                20                  25                  30

 Thr Val Ala Glu Leu Ala Thr Phe Pro Leu Asp Leu Thr Lys Thr
                35                  40                  45

 Arg Leu Gln Met Gln Gly Glu Ala Ala Leu Ala Arg Leu Gly Asp
                50                  55                  60

 Gly Ala Arg Glu Ser Ala Pro Tyr Arg Gly Met Val Arg Thr Ala
                65                  70                  75

 Leu Gly Ile Ile Glu Glu Glu Gly Phe Leu Lys Leu Trp Gln Gly
                80                  85                  90

 Val Thr Pro Ala Ile Tyr Arg His Val Val Tyr Ser Gly Gly Arg
                95                 100                 105

 Met Val Thr Tyr Glu His Leu Arg Glu Val Val Phe Gly Lys Ser
               110                 115                 120

 Glu Asp Glu His Tyr Pro Leu Trp Lys Ser Val Ile Gly Gly Met
               125                 130                 135

 Met Ala Gly Val Ile Gly Gln Phe Leu Ala Asn Pro Thr Asp Leu
               140                 145                 150
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Val Lys Val Gln Met Gln Met Glu Gly Lys Arg Lys Leu Glu Gly
155 160 165

Lys Pro Leu Arg Phe Arg Gly Val His His Ala Phe Ala Lys Ile
170 175 180

Leu Ala Glu Gly Gly Ile Arg Gly Leu Trp Ala Gly Trp Val Pro
185 190 195

Asn Ile Gln Arg Ala Ala Leu Val Asn Met Gly Asp Leu Thr Thr
200 205 210

Tyr Asp Thr Val Lys His Tyr Leu Val Leu Asn Thr Pro Leu Glu
215 220 225

Asp Asn Ile Met Thr His Gly Leu Ser Ser Leu Cys Ser Gly Leu
230 235 240

Val Ala Ser Ile Leu Gly Thr Pro Ala Asp Val Ile Lys Ser Arg
245 250 255

Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr
260 265 270

Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly
275 280 285

Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met
290 295 300

Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg
305 310 315

Glu Met Ser Gly Val Ser Pro Phe
320

<210> 2
<211> 1039
<212> DNA
<213> Homo sapiens

<400> 2
ccgagctcgg atcccgttat cgtcttgcgc tactgctgaa tgtccgtccc 50

ggaggaggag gagaggcttt tgccgctgac ccagagatgg ccccgagcga 100

gcaaattcct actgtccggc tgcgcggcta ccgtggccga gctagcaacc 150

tttcccctgg atctcacaaa aactcgactc caaatgcaag gagaagcagc 200

tcttgctcgg ttgggagacg gtgcaagaga atctgccccc tataggggaa 250

tggtgcgcac agccctaggg atcattgaag aggaaggctt tctaaagctt 300

tggcaaggag tgacacccgc catttacaga cacgtagtgt attctggagg 350

tcgaatggtc acatatgaac atctccgaga ggttgtgttt ggcaaaagtg 400

aagatgagca ttatcccctt tggaaatcag tcattggagg gatgatggct 450

ggtgttattg gccagttttt agccaatcca actgacctag tgaaggttca 500

gatgcaaatg gaaggaaaaa ggaaactgga aggaaaacca ttgcgatttc 550

gtggtgtaca tcatgcattt gcaaaaatct tagctgaagg aggaatacga 600

gggctttggg caggctgggt acccaatata caaagagcag cactggtgaa 650

tatgggagat ttaaccactt atgatacagt gaaacactac ttggtattga 700

atacaccact tgaggacaat atcatgactc acggtttatc aagtttatgt 750

tctggactgg tagcttctat tctgggaaca ccagccgatg tcatcaaaag 800

cagaataatg aatcaaccac gagataaaca aggaagggga cttttgtata 850

aatcatcgac tgactgcttg attcaggctg ttcaaggtga aggattcatg 900

agtctatata aaggcttttt accatcttgg ctgagaatga ccccttggtc 950

aatggtgttc tggcttactt atgaaaaaat cagagagatg agtggagtca 1000

gtccatttta agaattctgc agatatccat cacactggc 1039

<210> 3
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence is synthesized

<400> 3
cgcggatccc gttatcgtct tgcgctactg c 31

<210> 4
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer

<400> 4
gcggaattct taaaatggac tgactccact catc 34

<210> 5
<211> 1248
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence is synthesized

<220>
<221> unsure
<222> 1231
<223> unknown base

<400> 5
cgttatcgtc ttgcgctact gctgaatgtc cgtcccggag gaggaggaga 50

ggcttttgcc gctgacccag agatggcccc gagcgagcaa attcctactg 100

tccggctgcg cggctaccgt ggccgagcta gcaacctttc ccctggatct 150

cacaaaaact cgactccaaa tgcaaggaga agcagctctt gctcggttgg 200

gagacggtgc aagagaatct gccccctata ggggaatggt gcgcacagcc 250

ctagggatca ttgaagagga aggctttcta aagctttggc aaggagtgac 300

acccgccatt tacagacacg tagttatttc tggaggtcga atggtcacat 350

atgaacatct ccgagaggtt gtgtttggca aaagtgaaga tgagcattat 400

ccccttttgga aatcagtcat tggagggatg atggctggtg ttattggcca 450

gtttttagcc aatccaactg acctagtgaa ggttcagatg caaatggaag 500

gaaaaaggaa actggaagga aaaccattgc gatttcgtgg tgtacatcat 550

gcatttgcaa aaatcttagc tgaaggagga atacgaaggc tttgggcagg 600

ctgggtaccc aatatacaaa gagcagcact ggtgaatatg ggagatttaa 650

ccacttatga tacagtgaaa cactacttgg tattgaatac accacttgag 700

gacaatatca tgactcacgg tttatcaagt ttatgttctg gactggtagc 750

ttctattctg ggaacaccag ccgatgtcat caaaagcaga ataatgaatc 800

aaccacgaga taaacaagga aggggacttt tgtataaatc atcgactgac 850

tgcttgattc aggctgttca aggtgaagga ttcatgagtc tatataaagg 900

ctttttacca tcttggctga gaatgacccc ttggtcaatg gtgttctggc 950

ttacttatga aaaaatcaga gagatgagtg gagtcagtcc attttaaacc 1000

cctaaagatg caacccttaa agatacagtg ttcagtatta ttgaaatatg 1050

ggcatctgca acacataccc cctattattt ctacctcttt aggaagacac 1100

ctattccaca gagactgatt tatagggggc agcactttat ttttttctgg 1150

aaacccaagt tctctttgac tcctcttttt gtccaaaagt gatctggtcg 1200

gatctcacaa ggccatccaa tgagaccccg nacagcattt tctaaaga 1248

<210> 6
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence is synthesized

<400> 6
cgcggatccg aaatggacta caaggacgac gatgacaagt ccgtcccgga 50

ggaggagg 58

<210> 7
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence is synthesized

<400> 7
gcgaagcttg ccatggttgg actgaagcct tcaga 35

<210> 8
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer

<400> 8
cgcgaattct caaaacggtg attcccgtaa cat 33

<210> 9
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence is synthesized

<400> 9
gcgaagcttg ccatggacta caaggacgac gatgacaagg ttggactgaa 50

gccttcagac g 61

<210> 10
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence is synthesized

<400> 10
aatgcctatc gccgaggag 19

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer

<400> 11
gtaggaactt gctcgtccgg 20

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence is synthesized

<400> 12
tgctcgcgct cacgcagaga tg 22

<210> 13
<211> 24
<212> DNA

<213> Artificial Sequence

<220>
<223> Sequence is synthesized

<400> 13
gaaatcgtgc gtgacatcaa agag 24

<210> 14
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer

<400> 14
ctccttctgc atcctgtcag caa 23

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence is synthesized

<400> 15
cggttccgat gccctgaggc tc 22

<210> 16
<211> 307
<212> PRT
<213> Homo sapiens

<400> 16

Met	Gly	Gly	Leu	Thr	Ala	Ser	Asp	Val	His	Pro	Thr	Leu	Gly	Val
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Gln	Leu	Phe	Ser	Ala	Pro	Ile	Ala	Ala	Cys	Leu	Ala	Asp	Val	Ile
				20				25						30
Thr	Phe	Pro	Leu	Asp	Thr	Ala	Lys	Val	Arg	Leu	Gln	Val	Gln	Gly
				35				40						45
Glu	Cys	Pro	Thr	Ser	Ser	Val	Ile	Arg	Tyr	Lys	Gly	Val	Leu	Gly
				50				55						60
Thr	Ile	Thr	Ala	Val	Val	Lys	Thr	Glu	Gly	Arg	Met	Lys	Leu	Tyr
				65				70						75
Ser	Gly	Leu	Pro	Ala	Gly	Leu	Gln	Arg	Gln	Ile	Ser	Ser	Ala	Ser
				80				85						90
Leu	Arg	Ile	Gly	Leu	Tyr	Asp	Thr	Val	Gln	Glu	Phe	Leu	Thr	Ala
				95				100						105
Gly	Lys	Glu	Thr	Ala	Pro	Ser	Leu	Gly	Ser	Lys	Ile	Leu	Ala	Gly
				110				115						120
Leu	Thr	Thr	Gly	Gly	Val	Ala	Val	Phe	Ile	Gly	Gln	Pro	Thr	Glu
				125				130						135

Val Val Lys Val Arg Leu Gln Ala Gln Ser His Leu His Gly Ile
140 145 150

Lys Pro Arg Tyr Thr Gly Thr Tyr Asn Ala Tyr Arg Ile Ile Ala
155 160 165

Thr Thr Glu Gly Leu Thr Gly Leu Trp Lys Gly Thr Thr Pro Asn
170 175 180

Leu Met Arg Ser Val Ile Ile Asn Cys Thr Glu Leu Val Thr Tyr
185 190 195

Asp Leu Met Lys Glu Ala Phe Val Lys Asn Asn Ile Leu Ala Asp
200 205 210

Asp Val Pro Cys His Leu Val Ser Ala Leu Ile Ala Gly Phe Cys
215 220 225

Ala Thr Ala Met Ser Ser Pro Val Asp Val Val Lys Thr Arg Phe
230 235 240

Ile Asn Ser Pro Pro Gly Gln Tyr Lys Ser Val Pro Asn Cys Ala
245 250 255

Met Lys Val Phe Thr Asn Glu Gly Pro Thr Ala Phe Phe Lys Gly
260 265 270

Leu Val Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val Ile Met
275 280 285

Phe Val Cys Phe Glu Gln Leu Lys Arg Glu Leu Ser Lys Ser Arg
290 295 300

Gln Thr Met Asp Cys Ala Thr
305

<210> 17
<211> 309
<212> PRT
<213> Homo sapiens

<400> 17
Met Val Gly Phe Lys Ala Thr Asp Val Pro Pro Thr Ala Thr Val
1 5 10 15

Lys Phe Leu Gly Ala Gly Thr Ala Ala Cys Ile Ala Asp Leu Ile
20 25 30

Thr Phe Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly
35 40 45

Glu Ser Gln Gly Pro Val Arg Ala Thr Val Ser Ala Gln Tyr Arg
50 55 60

Gly Val Met Gly Thr Ile Leu Thr Met Val Arg Thr Glu Gly Pro
65 70 75

Arg Ser Leu Tyr Asn Gly Leu Val Ala Gly Leu Gln Arg Gln Met
80 85 90

Ser Phe Ala Ser Val Arg Ile Gly Leu Tyr Asp Ser Val Lys Gln
95 100 105

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Phe Tyr Thr Lys Gly Ser Glu His Ala Ser Ile Gly Ser Arg Leu
                110                 115                 120

Leu Ala Gly Ser Thr Thr Gly Ala Leu Ala Val Ala Val Ala Gln
                125                 130                 135

Pro Thr Asp Val Val Lys Val Arg Phe Gln Ala Gln Ala Arg Ala
                140                 145                 150

Gly Gly Gly Arg Arg Tyr Gln Ser Thr Val Asn Ala Tyr Lys Thr
                155                 160                 165

Ile Ala Arg Glu Glu Gly Phe Arg Gly Leu Trp Lys Gly Thr Ser
                170                 175                 180

Pro Asn Val Ala Arg Asn Ala Ile Val Asn Cys Ala Glu Leu Val
                185                 190                 195

Thr Tyr Asp Leu Ile Lys Asp Ala Leu Leu Lys Ala Asn Leu Met
                200                 205                 210

Thr Asp Asp Leu Pro Cys His Phe Thr Ser Ala Phe Gly Ala Gly
                215                 220                 225

Phe Cys Thr Thr Val Ile Ala Ser Pro Val Asp Val Val Lys Thr
                230                 235                 240

Arg Tyr Met Asn Ser Ala Leu Gly Gln Tyr Ser Ser Ala Gly His
                245                 250                 255

Cys Ala Leu Thr Met Leu Gln Lys Glu Gly Pro Arg Ala Phe Tyr
                260                 265                 270

Lys Gly Phe Met Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val
                275                 280                 285

Val Met Phe Val Thr Tyr Glu Gln Leu Lys Arg Ala Leu Met Ala
                290                 295                 300

Ala Cys Thr Ser Arg Glu Ala Pro Phe
                305
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<210> 18
<211> 300
<212> PRT
<213> Homo sapiens

<400> 18

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 Met Ala Val Lys Phe Leu Gly Ala Gly Thr Ala Ala Cys Phe Ala
   1               5                  10                  15

 Asp Leu Val Thr Phe Pro Leu Asp Thr Ala Lys Val Arg Leu Gln
                20                  25                  30

 Ile Gln Gly Glu Asn Gln Ala Val Gln Thr Ala Arg Leu Val Gln
                35                  40                  45

 Tyr Arg Gly Val Leu Gly Thr Ile Leu Thr Met Val Arg Thr Glu
                50                  55                  60

 Gly Pro Cys Ser Pro Tyr Asn Gly Leu Val Ala Gly Leu Gln Arg
                65                  70                  75
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Gln Met Ser Phe Ala Ser Ile Arg Ile Gly Leu Tyr Asp Ser Val
                80                  85                  90

Lys Gln Val Tyr Thr Pro Lys Gly Ala Asp Asn Ser Ser Leu Thr
                95                 100                 105

Thr Arg Ile Leu Ala Gly Cys Thr Thr Gly Ala Met Ala Val Thr
               110                 115                 120

Cys Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe Gln Ala Ser
               125                 130                 135

Ile His Leu Gly Pro Ser Arg Ser Asp Arg Lys Tyr Ser Gly Thr
               140                 145                 150

Met Asp Ala Tyr Arg Thr Ile Ala Arg Glu Glu Gly Val Arg Gly
               155                 160                 165

Leu Trp Lys Gly Thr Leu Pro Asn Ile Met Arg Asn Ala Ile Val
               170                 175                 180

Asn Cys Ala Glu Val Val Thr Tyr Asp Ile Leu Lys Glu Lys Leu
               185                 190                 195

Leu Asp Tyr His Leu Leu Thr Asp Asn Phe Pro Cys His Phe Val
               200                 205                 210

Ser Ala Phe Gly Ala Gly Phe Cys Ala Thr Val Val Ala Ser Pro
               215                 220                 225

Val Asp Val Val Lys Thr Arg Tyr Met Asn Ser Pro Pro Gly Gln
               230                 235                 240

Tyr Phe Ser Pro Leu Asp Cys Met Ile Lys Met Val Ala Gln Glu
               245                 250                 255

Gly Pro Thr Ala Phe Tyr Lys Gly Phe Thr Pro Ser Phe Leu Arg
               260                 265                 270

Leu Gly Ser Trp Asn Val Val Met Phe Val Thr Tyr Glu Gln Leu
               275                 280                 285

Lys Arg Ala Leu Met Lys Val Gln Met Leu Arg Glu Ser Pro Phe
               290                 295                 300
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